

# SEQUENCE LISTING

<110> Choe, Sunghwa  
Feldmann, Kenneth A

<120> Dwf7 MUTANTS

<130> 2225-0003

<140> 09/775,879

<141> 2001-02-02

<150> 60/179,901

<151> 2000-02-02

<160> 25

<170> PatentIn Ver. 2.0

<210> 1

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer S5D\_FF

<400> 1

cagtgtgagt aatttagcat tacta

25

<210> 2

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer S5D\_LR

<400> 2

ggaaagatca tcaaacattt acatgt

26

<210> 3

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer S5D\_1F

<400> 3

gcgcaatctt ctttcgttt

19

<210> 4

<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer S5D\_1R

<400> 4  
tggacaacaa caacacaaga

20

<210> 5  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer S5D\_2F

<400> 5  
gatgcacaga gagcttcacg ac

22

<210> 6  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer S5D\_2R

<400> 6  
ccggcaaagt gagagagtg at

22

<210> 7  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer S5D\_3F

<400> 7  
caccatcat atctacaaca a

21

<210> 8  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer S5D\_4F

<400> 8  
catcttttgc cggcgaatct at

22

<210> 9

<211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer D7-5-1  
  
 <400> 9 32-  
 gtagaagcac cagaggaaac cggagatgaa gt  
  
 <210> 10  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer D7-5-2  
  
 <400> 10 26  
 aagtatagta gggttccggc gaggta  
  
 <210> 11  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer D7-5-3  
  
 <400> 11 26  
 atagattcgc cggcaaaaga tgactc  
  
 <210> 12  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer D7-3-1  
  
 <400> 12 32  
 tgcaggatac catacagatac accacacgac at  
  
 <210> 13  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer D7-3-2  
  
 <400> 13 35  
 catacagatac accacacgac atacaagcat aacta

<210> 14  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer D7-3-3

<400> 14  
 atatggatgg attggatgtt tggctctc

28

<210> 15  
 <211> 364  
 <212> PRT  
 <213> delta-7 sterol C-5 desaturase (Candida glabrata)

<400> 15  
 Met Asp Leu Val Leu Glu Thr Leu Asp His Tyr Ile Phe Asp Asp Val  
           1                  5                  10                  15  
 Tyr Ala Lys Ile Ala Pro Val Glu Leu Gln Arg Gly Ile Asp Asp Ser  
                   20                  25                  30  
 Leu Val Asn Ala Leu Ser Leu Asn Lys Ile Val Ser Asn Ser Thr Leu  
                   35                  40                  45  
 Leu His Glu Thr Leu Ser Ile Thr Asn Ser Leu Lys Arg Val Asn Lys  
                   50                  55                  60  
 Asp Val Tyr Gly Leu Thr Pro Phe Leu Phe Asp Phe Thr Glu Lys Thr  
                   65                  70                  75                  80  
 Tyr Ala Ser Leu Leu Pro Arg Asn Asn Leu Ile Arg Glu Phe Phe Ser  
                   85                  90                  95  
 Leu Trp Ala Val Val Thr Val Phe Gly Leu Leu Leu Tyr Leu Ile Thr  
                   100                  105                  110  
 Ala Ser Leu Ser Tyr Val Phe Val Phe Asp Arg Thr Ile Phe Asn His  
                   115                  120                  125  
 Pro Lys Tyr Leu Lys Asn Gln Met Tyr Leu Glu Ile Lys Leu Ala Val  
                   130                  135                  140  
 Ser Ala Ile Pro Thr Met Ser Leu Leu Thr Val Pro Trp Phe Met Leu  
                   145                  150                  155                  160  
 Glu Leu Asn Gly Tyr Ser Lys Leu Tyr Tyr Asp Val Asp Trp Glu His  
                   165                  170                  175  
 His Gly Leu Arg Lys Leu Leu Ile Glu Tyr Ala Thr Phe Ile Phe Phe  
                   180                  185                  190  
 Thr Asp Cys Gly Ile Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg

195	200	205
Val Tyr Lys Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr		
210	215	220
Pro Phe Ala Ser His Ala Phe His Pro Val Asp Gly Tyr Phe Gln Ser		
225	230	235 240
Leu Ser Tyr His Ile Tyr Pro Met Ile Leu Pro Leu His Lys Ile Ser		
	245	250 255
Tyr Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Ser Val Met Ile His		
	260	265 270
Asp Gly Gln His Met Ser Asn Asn Pro Val Val Asn Gly Thr Ala Cys		
	275	280 285
His Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr		
	290	295 300
Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Glu Asp Ser		
	305	310 315 320
Leu Phe Asp Pro Lys Leu Lys Met Asp Lys Lys Val Leu Glu Lys Gln		
	325	330 335
Ala Arg Glu Thr Ala Ala Tyr Ile Gln Glu Val Glu Gly Asp Asp Thr		
	340	345 350
Asp Arg Val Tyr Asn Thr Asp Lys Lys Lys Thr Asn		
	355	360
<210> 16		
<211> 365		
<212> PRT		
<213> delta-7 sterol C-5 desaturase (Saccharomyces cerevisiae)		
<400> 16		
Met Asp Leu Val Leu Glu Val Ala Asp His Tyr Val Leu Asp Asp Leu		
1	5	10 15
Tyr Ala Lys Val Leu Pro Ala Ser Leu Ala Ala Asn Ile Pro Val Lys		
	20	25 30
Trp Gln Lys Leu Leu Gly Leu Asn Ser Gly Phe Ser Asn Ser Thr Ile		
	35	40 45
Leu Gln Glu Thr Leu Asn Ser Lys Asn Ala Val Lys Glu Cys Arg Arg		
	50	55 60
Phe Tyr Gly Gln Val Pro Phe Leu Phe Asp Met Ser Thr Thr Ser Phe		
	65	70 75 80

Ala Ser Leu Leu Pro Arg Ser Ser Ile Leu Arg Glu Phe Leu Ser Leu  
 85 90 95  
 Trp Val Ile Val Thr Ile Phe Gly Leu Leu Tyr Leu Phe Thr Ala  
 100 105 110  
 Ser Leu Ser Tyr Val Phe Val Phe Asp Lys Ser Ile Phe Asn His Pro  
 115 120 125  
 Arg Tyr Leu Lys Asn Gln Met Ala Met Glu Ile Lys Leu Ala Val Ser  
 130 135 140  
 Ala Ile Pro Trp Met Ser Met Leu Thr Val Pro Trp Phe Val Met Glu  
 145 150 155 160  
 Leu Asn Gly His Ser Lys Leu Tyr Met Lys Ile Asp Tyr Glu Asn His  
 165 170 175  
 Gly Val Arg Lys Leu Ile Ile Glu Tyr Phe Thr Phe Ile Phe Phe Thr  
 180 185 190  
 Asp Cys Gly Val Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg Val  
 195 200 205  
 Tyr Arg Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro  
 210 215 220  
 Phe Ala Ser His Ser Phe His Pro Val Asp Gly Phe Leu Gln Ser Ile  
 225 230 235 240  
 Ser Tyr His Ile Tyr Pro Leu Ile Leu Pro Leu His Lys Val Ser Tyr  
 245 250 255  
 Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Thr Val Met Ile His Asp  
 260 265 270  
 Gly Gln Tyr Leu Ser Asn Asn Pro Ala Val Asn Gly Thr Ala Cys His  
 275 280 285  
 Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr Thr  
 290 295 300  
 Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Asp Asp Ser Leu  
 305 310 315 320  
 Phe Asp Pro Lys Leu Arg Asp Ala Lys Glu Thr Trp Asp Ala Gln Val  
 325 330 335  
 Lys Glu Val Glu His Phe Ile Lys Glu Val Glu Gly Asp Asp Asn Asp  
 340 345 350  
 Arg Ile Tyr Glu Asn Asp Pro Asn Thr Lys Lys Asn Asn  
 355 360 365

<210> 17

<211> 329

<212> PRT

<213> delta-7 sterol C-5 desaturase (Schizosaccharomyces pombe)

<400> 17

Met Asp Val Val Leu Gln Tyr Ala Asp Lys Tyr Val Phe Asp Thr Phe  
1 5 10 15

Tyr Gly Lys Ile Ala Glu Ser Phe Asp Ser Ser Ser Ser Phe Ala Asn  
20 25 30

Thr Ala Val Asn Ser Thr Thr Leu Gly Leu Ala Glu Lys Val Asn Phe  
35 40 45

Ala Ile Thr Ser Gly Leu Leu Asp Arg Asn Asn Val Trp Arg Gln Phe  
50 55 60

Thr Ser Leu Phe Leu Ile Thr Trp Ile Met Gly Thr Leu Ser Tyr Phe  
65 70 75 80

Leu Ser Ala Ser Phe Ala Tyr Tyr Val Tyr Phe Asp Arg Glu Glu Ala  
85 90 95

Arg Arg His Pro Lys Phe Leu Lys Asn Gln Glu His Leu Glu Leu Met  
100 105 110

Val Ala Leu Lys Asn Leu Pro Gly Met Ala Ile Leu Thr Ala Pro Trp  
115 120 125

Phe Leu Ala Glu Ile Arg Gly Tyr Gly Tyr Val Tyr Asp Lys Leu Asp  
130 135 140

Glu Tyr Gly Tyr Phe Tyr Leu Phe Phe Ser Ile Ala Leu Phe Leu Leu  
145 150 155 160

Phe Ser Asp Phe Leu Ile Tyr Trp Ile His Arg Ala Leu His His Arg  
165 170 175

Trp Leu Tyr Ala Pro Leu His Lys Leu His His Lys Trp Ile Val Pro  
180 185 190

Thr Pro Tyr Ser Ser His Ala Phe His Tyr Leu Asp Gly Tyr Ser Gln  
195 200 205

Ser Leu Pro Tyr His Met Phe Pro Phe Phe Phe Pro Leu Asn Lys Tyr  
210 215 220

Val Tyr Leu Leu Leu Phe Gly Ser Val Asn Tyr Trp Thr Val Leu Ile  
225 230 235 240

His Asp Gly Lys Tyr Phe Ser Asn Asn Ala Val Val Asn Gly Ala Ala  
245 250 255

His His Ala Ala His His Met Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe  
 260 265 270

Phe Thr Leu Phe Asp Arg Leu Cys Ser Ser Tyr Arg Gln Pro Asp Gln  
 275 280 285

Glu Leu Phe Asp Ala Glu Leu Arg Asn Glu Lys Leu Gln Glu Gln Arg  
 290 295 300

Ile Arg Phe Met Glu Thr Val Gln Tyr Thr Val Glu Gly Lys Asp Asp  
 305 310 315 320

Arg Thr Tyr Ala Ser Lys Lys Asp Asn  
 325

<210> 18

<211> 281

<212> PRT

<213> DWF7/STE1 (Arabidopsis)

<400> 18

Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser  
 1 5 10 15

Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp  
 20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala  
 35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile  
 50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr  
 65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro  
 85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly  
 100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr  
 115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr  
 130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu  
 145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe  
 165 170 175



Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro  
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile  
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys  
210 215 220

Ile His Gly Asn Ile Trp Pro Val Met Gly Ala Gly Tyr His Thr Ile  
225 230 235 240

His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met  
245 250 255

Asp Trp Met Phe Gly Ser Leu Arg Asp Pro Leu Leu Glu Glu Asp Asp  
260 265 270

Asn Lys Asp Ser Phe Lys Lys Ala Glu  
275 280

<210> 19  
<211> 291  
<212> PRT  
<213> delta-7 sterol C-5 desaturase concensus

<400> 19  
Met Asp Leu Val Leu Glu Ala Asp His Tyr Val Phe Asp Asp Tyr Ala  
1 5 10 15

Lys Ile Pro Leu Ala Ile Asp Ser Leu Leu Asn Val Ser Asn Ser Thr  
20 25 30

Leu Glu Thr Leu Asn Lys Val Asn Tyr Gly Pro Phe Leu Phe Asp Phe  
35 40 45

Thr Glu Thr Ser Phe Ser Leu Leu Pro Arg Asn Asn Leu Trp Arg Glu  
50 55 60

Phe Leu Ser Leu Trp Leu Ile Val Thr Ile Phe Gly Leu Leu Tyr Ile  
65 70 75 80

Ala Ser Leu Ser Tyr Phe Phe Asp Ile Phe Asn His Pro Lys Tyr Leu  
85 90 95

Lys Asn Gln Met Leu Glu Ile Lys Ala Val Ala Ile Pro Trp Met Ser  
100 105 110

Leu Leu Thr Val Pro Trp Phe Met Glu Leu Gly Tyr Ser Lys Leu Tyr  
115 120 125

Lys Ile Asp Glu His Gly Arg Lys Leu Phe Ile Glu Ala Thr Phe Phe  
130 135 140

Phe Thr Asp Gly Ile Tyr Ala His Arg Trp Leu His Trp Pro Tyr Lys  
 145 150 155 160  
 Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro Phe Ala  
 165 170 175  
 Ser His Ala Phe His Pro Val Asp Gly Tyr Leu Gln Ser Leu Tyr His  
 180 185 190  
 Ile Tyr Pro Leu Leu Pro Leu His Lys Ser Tyr Leu Leu Phe Thr Phe  
 195 200 205  
 Val Asn Phe Trp Thr Val Met Ile His Asp Gly Gln Ser Asn Asn Pro  
 210 215 220  
 Val Val Asn Gly Ala Cys His Thr Val His His Leu Tyr Phe Asn Tyr  
 225 230 235 240  
 Asn Tyr Gly Gln Phe Thr Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr  
 245 250 255  
 Arg Arg Pro Asp Ser Leu Phe Asp Pro Lys Leu Arg Asp Lys Lys Glu  
 260 265 270  
 Gln Arg Glu Thr Tyr Ile Glu Val Glu Gly Asp Asp Asp Arg Tyr Asp  
 275 280 285  
 Lys Lys Asn  
 290

<210> 20  
 <211> 1889  
 <212> DNA  
 <213> Genomic dwf7 (Arabidopsis)

<400> 20  
 gaagatcgat caatcaatca tcaaactctc tgtgtgccac atgcattact actgttgact 60  
 tgttcaataa aggtaaagta agatcaatcc ggcgaatctt ctttcgtttt ccggcaccga 120  
 tctcgggtgga tctccgattc acatggcggc ggataatgct tatctgatgc agtttggtga 180  
 cgaaacctct ttttacaacc gaatcggtct gagtcatctt ttgccggcga atctatggga 240  
 acccttacct cattttctcc agacatggct ccgaaattac ctgcgcggaa ccctactata 300  
 cttcatctcc gggttcctct ggtgcttcta catctattac cttaaaatca acgtttacct 360  
 tcccaaagggt ctgcactttc acttttgtat tcactattgc ttaatcgctt tctatgttat 420  
 cgatttttca atttaaggaa gaggggttct tcgtgtactg tacagtaatt tggatttgat 480  
 gtggatagtt catgtttgca tttattgatt atttgtgcat attctccatc taagggattg 540  
 aacagttagt ggcttatata agtttttgtg caaccaatga gaagtcgtac atctttgaag 600  
 ttgaattttc tacttgccat ttaagtccac ttaaattgtt tgttgaaagt attgtctact 660  
 ttcagacaca ttctttttct gcttctctga gactctgtct tagtttgaaa tcttttttgg 720  
 tctgttttgc ttcagatgca attcctacaa taaaggctat gcgtttgcaa atgtttgtgg 780  
 caatgaaggc tatgccatgg tacactcttc ttccaactgt ctccgagagt atgattgaac 840  
 gtggttgagc caaatgtttt gctagcatag acgaattcgg ctggattctg tattttgttt 900  
 acatcgccat ctatcttggt ttcggttgagt ttggtattta ttggatgcac agagagcttc 960  
 atgacattaa gcctctctat aagtatctcc atgccacca tcatatctac aacaagcaga 1020

atacactctc tccatttgcc ggtaagtgtt ttcagtttgt tcttcttttag ttcttgtaaa 1080  
 agattggttag catttagttt cttaccagaa aagactttgt cagcagctgc ttgtactcca 1140  
 aatcacattt tgcattcctt atccataaag taaccagaaa ggctagaatt atataaatgt 1200  
 cagctgcatt acttcacata tgtcagagag acttctgact taaccagagt ttagatcttt 1260  
 gtgtttctct tctgggtctcg gactgattgg aaatgacgag aagttctttt atctacttcc 1320  
 ctggagtgtg tcttggttaa tccaaggatg tgacatctaa tattacttgt aacttcctta 1380  
 cgtttttggt tacagggcct gcatttcacc cagtagacgg gatacttcag gctgtaccgc 1440  
 atgtgatagc gctgtttata gtgccaatc atttcacaac tcatataggt cttttgttca 1500  
 tgggaagcgt atggacggcg aacatccatg actgcatcca tggcaacatc tggccagtaa 1560  
 tgggtgcagg ataccatacg atacaccaca cgacatacaa gcataactat ggtcattata 1620  
 ccatatggat ggattggatg tttggctctc ttagggatcc tctcttagaa gaagatgaca 1680  
 acaaagacag cttcaagaaa gcagagttag aatgccact tgggttttgt tcttctgttt 1740  
 tgtcttgtgt tgttgttgtt caaagtttca gcctttcttg ttctttttct tcttcttctt 1800  
 attcatgtgt ctctctcaac ctttccaatt atattgttac aaacatttgc tgtctagttt 1860  
 aaaacatgta aatgtttgat gatctttgc 1999

<210> 21  
 <211> 281  
 <212> PRT  
 <213> DWF7

<400> 21

Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser  
 1 5 10 15

Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp  
 20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala  
 35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile  
 50 55 60

Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr  
 65 70 75 80

Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro  
 85 90 95

Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly  
 100 105 110

Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr  
 115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr  
 130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu  
 145 150 155 160

His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe  
 165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro  
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile  
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys  
210 215 220

Ile His Gly Asn Ile Trp Pro Val Met Gly Ala Gly Tyr His Thr Ile  
225 230 235 240

His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met  
245 250 255

Asp Trp Met Phe Gly Ser Leu Arg Asp Pro Leu Leu Glu Glu Asp Asp  
260 265 270

Asn Lys Asp Ser Phe Lys Lys Ala Glu  
275 280

<210> 22  
<211> 2925  
<212> DNA  
<213> Genomic HDF7

<400> 22  
gtttggtatt tattggatgc acagagagct tcatgacatt aagcctctct ataagtatct 60  
ccatgccacc catcatatct acaacaagca gaatacactc tctccatttg cgggtaagtg 120  
ttttcagttt gttcttcttt agttcttgta aaagattggg agcatttagt ttcttaccag 180  
aaaagacttt gtcagcagct gcttgactc caaatcacat tttgcattcc ttatccataa 240  
agtaaccaga aaggctagaa ttatataaat gtcagctgca ttacttcaca tatgtcagag 300  
agacttctga cttaaccaga gtttagatct ttgtgtttct cttctgggtc cggactgatt 360  
ggaaatgacg agaagttctt ttatctactt ccctggagtg tatcttgggt aatccaagga 420  
tgtgacatct aaatattact tgtaacttcc ttacgttttt gtttacaggg cttgcattca 480  
cccagtagac gggatactta aggtgttacc gcatgtgata gcgctgttat agtgccaatt 540  
catttcacaa ctcatatagg tcttttggtc atggaagcga tatggacggc gaacatccat 600  
gactgcatcc atggcaacat ctggccagta atgggtgcag gataccatac gatacaccac 660  
acgacataca agcataacta tggtcattat accatatgga tggattggat gtttgggtct 720  
cttagggatc ctctcttaga agaagatgac acaaaagaca gcttcaagaa agcagagtga 780  
gaatgcccac ttgggttttg ttcttctgtt ttgtcttggt ttgttgttgt tcaaagtttc 840  
agcctttctt gttctttttc ttcttcttct tattcatgtg tctctctcaa cctttccaat 900  
tatattgtta caaacatttg ctgtctagt taaaacatgt aaatgtttga tgatctttgc 960  
aagactccat ttttgtttaa ggtaaacctt gaatctcata gattgtcgat tgttgggtatt 1020  
tccattttca ggtacgggtc ttagactgt agtcttgctg accagtccgg cttaaccacc 1080  
ccaaatttca aagatctcac caatcaaaat gctggctggc cccaatatat agatgggcca 1140  
gttaatccgt ctagctttac tcttttagacc taccttagac agttagacac ctgctaatta 1200  
atgagtttcc tttttcttgt tcagcaagtt acctgtgtta cttgagagtt gagttaatgg 1260  
tagtaaacgc aatttaacc ttataagttt aatcgattc aacgaatgac ccagagactt 1320  
taaataaatc catcgtaacc ctccacttca aaattctttt taaaaagtag caaatcattt 1380  
aaatattgta agtttgcttc attcgaaatt gtagctacag atctcaaagc tctctctgtt 1440  
ggccatatct ctctctaaca aacgcatagt aacacttgac cacagtttga cttctcggcg 1500  
gtttcatggc ggcgactatg gcagattata atgatcagat cgtcaatgag acctcttttt 1560

```

acaaccgaat ggttctgagt caccttttgc cgggtgaatct atgggaacct ttaccacatt 1620
tcctccagac atgggtccgg aactacctcg ccggaaacat actctacttc atctccggct 1680
tcctctgggtg cttctacatc tattacctta aactcaacgt ttacgtcccc aaaggttact 1740
tttttcaatt tcgatgttct gttttgaaac ctttcttttg ttgattcctt cgattgtatc 1800
gcctgataga ttgtgttata cgttaacctt tttttcttac tgttactttc agttcttgtc 1860
ttctactttc catttaatta gttttaaaagt ttaatatatt tggctaatac acatttttta 1920
agttgaatct tccatgaaat ttgagctcaa aatataccat gaaattgaaa tttgtgggtc 1980
ttagttctat ttcttgcttg gtttcttcta tttttgtggt tagaatccat tcctacgaga 2040
aaggcaatgc ttttgcaa atacgtggca atgaaggcta tgccttggtg cactcttctt 2100
ccagctgtct ctgagtatat gatcgagcat ggttggaaca aatgttactc tacacttgac 2160
catttcaact ggttcctctg tttcctctac atagctctct atcttgtttt agttgagttt 2220
atgatttatt ggggtcacaa agagcttcat gacattaaat ttctctataa gcatctccat 2280
gctacccatc atagtataca caagcaaaac acactctctc catttgccgg tatgtcaaag 2340
ctatatgttc tcaatctaaa ttcaagagct tgtatcaatg gtgacttctt tacttgatgt 2400
ttttcgggtt ttcagggtc gcattccatc cgctggacgg gatacttcag gctataccgc 2460
acgtgatagc gctgtttata gtgccgattc atctcataac acatctgagt cttttgtttt 2520
tggaagggat atggacagca agcatccatg attgcataca tggtaacatc tggcctataa 2580
tggtgacagg ataccatacc atacaccata caacatacaa gcataactat ggtcattata 2640
ccatatggat ggactggatg tttggctctc ttatgggtcc tttagcagaa aaagacagtt 2700
tcaaggagaa agaaaagtga gaatgttcaa tgctcacatg tattcttcat atgttgctct 2760
tctcgtgact cttattaaaa cttttcta at cactttggtg gaattaaaaa catgactgca 2820
taatttgatg caaagtttca gacttttatt gctaaaaatc tctgatgatt attaacctca 2880
attatataat tgctggatga agagttcaaa tttggactaa atctg 2925

```

<210> 23  
 <211> 279  
 <212> PRT  
 <213> HDF7

<400> 23  
 Met Ala Ala Thr Met Ala Asp Tyr Asn Asp Gln Ile Val Asn Glu Thr  
 1 5 10 15  
 Ser Phe Tyr Asn Arg Met Val Leu Ser His Leu Leu Pro Val Asn Leu  
 20 25 30  
 Trp Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu  
 35 40 45  
 Ala Gly Asn Ile Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr  
 50 55 60  
 Ile Tyr Tyr Leu Lys Leu Asn Val Tyr Val Pro Lys Glu Ser Ile Pro  
 65 70 75 80  
 Thr Arg Lys Ala Met Leu Leu Gln Ile Tyr Val Ala Met Lys Ala Met  
 85 90 95  
 Pro Trp Tyr Thr Leu Leu Pro Ala Val Ser Glu Tyr Met Ile Glu His  
 100 105 110  
 Gly Trp Thr Lys Cys Tyr Ser Thr Leu Asp His Phe Asn Trp Phe Leu  
 115 120 125

Cys Phe Leu Tyr Ile Ala Leu Tyr Leu Val Leu Val Glu Phe Met Ile  
 130 135 140

Tyr Trp Val His Lys Glu Leu His Asp Ile Lys Phe Leu Tyr Lys His  
 145 150 155 160

Leu His Ala Thr His His Met Tyr Asn Lys Gln Asn Thr Leu Ser Pro  
 165 170 175

Phe Ala Gly Leu Ala Phe His Pro Leu Asp Gly Ile Leu Gln Ala Ile  
 180 185 190

Pro His Val Ile Ala Leu Phe Ile Val Pro Ile His Leu Ile Thr His  
 195 200 205

Leu Ser Leu Leu Phe Leu Glu Gly Ile Trp Thr Ala Ser Ile His Asp  
 210 215 220

Cys Ile His Gly Asn Ile Trp Pro Ile Met Gly Ala Gly Tyr His Thr  
 225 230 235 240

Ile His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp  
 245 250 255

Met Asp Trp Met Phe Gly Ser Leu Met Val Pro Leu Ala Glu Lys Asp  
 260 265 270

Ser Phe Lys Glu Lys Glu Lys  
 275

<210> 24  
 <211> 60  
 <212> PRT  
 <213> dwf7-2

<400> 24  
 Met Ala Ala Asp Asn Ala Tyr Leu Met Gln Phe Val Asp Glu Thr Ser  
 1 5 10 15

Phe Tyr Asn Arg Ile Val Leu Ser His Leu Leu Pro Ala Asn Leu Trp  
 20 25 30

Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala  
 35 40 45

Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp  
 50 55 60

<210> 25  
 <211> 230  
 <212> PRT  
 <213> dwf7-1

<400> 25

Met	Ala	Ala	Asp	Asn	Ala	Tyr	Leu	Met	Gln	Phe	Val	Asp	Glu	Thr	Ser
1				5					10					15	
Phe	Tyr	Asn	Arg	Ile	Val	Leu	Ser	His	Leu	Leu	Pro	Ala	Asn	Leu	Trp
			20					25					30		
Glu	Pro	Leu	Pro	His	Phe	Leu	Gln	Thr	Trp	Leu	Arg	Asn	Tyr	Leu	Ala
		35					40					45			
Gly	Thr	Leu	Leu	Tyr	Phe	Ile	Ser	Gly	Phe	Leu	Trp	Cys	Phe	Tyr	Ile
	50					55					60				
Tyr	Tyr	Leu	Lys	Ile	Asn	Val	Tyr	Leu	Pro	Lys	Asp	Ala	Ile	Pro	Thr
65					70					75					80
Ile	Lys	Ala	Met	Arg	Leu	Gln	Met	Phe	Val	Ala	Met	Lys	Ala	Met	Pro
				85					90						95
Trp	Tyr	Thr	Leu	Leu	Pro	Thr	Val	Ser	Glu	Ser	Met	Ile	Glu	Arg	Gly
			100					105					110		
Trp	Thr	Lys	Cys	Phe	Ala	Ser	Ile	Asp	Glu	Phe	Gly	Trp	Ile	Leu	Tyr
		115					120					125			
Phe	Val	Tyr	Ile	Ala	Ile	Tyr	Leu	Val	Phe	Val	Glu	Phe	Gly	Ile	Tyr
	130					135					140				
Trp	Met	His	Arg	Glu	Leu	His	Asp	Ile	Lys	Pro	Leu	Tyr	Lys	Tyr	Leu
145					150					155					160
His	Ala	Thr	His	His	Ile	Tyr	Asn	Lys	Gln	Asn	Thr	Leu	Ser	Pro	Phe
				165					170					175	
Ala	Gly	Leu	Ala	Phe	His	Pro	Val	Asp	Gly	Ile	Leu	Gln	Ala	Val	Pro
		180						185					190		
His	Val	Ile	Ala	Leu	Phe	Ile	Val	Pro	Ile	His	Phe	Thr	Thr	His	Ile
	195						200					205			
Gly	Leu	Leu	Phe	Met	Glu	Ala	Ile	Trp	Thr	Ala	Asn	Ile	His	Asp	Cys
	210					215					220				
Ile	His	Gly	Asn	Ile	Trp										
225					230										